



PCT

RAW SEQUENCE LISTING

DATE: 07/20/2004

PATENT APPLICATION: US/10/501,282

TIME: 11:37:49

Input Set : D:\Am100780.app

Output Set: N:\CRF4\07202004\J501282.raw

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3 <110> APPLICANT: MCMICHAEL, JOHN CALHOUN
4     ZAGURSKY, ROBERT JOHN
5     RUSSELL, DAVID PARRISH
6     FLETCHER, LEAH DIANE
8 <120> TITLE OF INVENTION: ALLOIOCOCCUS OTITIDIS OPEN READING FRAMES (ORFS) ENCODING
9     POLYPEPTIDE ANTIGENS, IMMUNOGENIC COMPOSITIONS AND USES THEREOF
11 <130> FILE REFERENCE: AM100780 L2
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/501,282
C--> 14 <141> CURRENT FILING DATE: 2004-07-09
16 <150> PRIOR APPLICATION NUMBER: 60/333,777
17 <151> PRIOR FILING DATE: 2001-11-29
19 <150> PRIOR APPLICATION NUMBER: 60/426,742
20 <151> PRIOR FILING DATE: 2002-11-18
22 <150> PRIOR APPLICATION NUMBER: PCT/US02/36123
23 <151> PRIOR FILING DATE: 2002-11-25
25 <160> NUMBER OF SEQ ID NOS: 6653
27 <170> SOFTWARE: PatentIn version 3.2
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 870
31 <212> TYPE: DNA
32 <213> ORGANISM: Alloiococcus otitidis
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (4)..(867)
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40 Met Met Asp Glu Arg Leu Thr Ser Leu Leu Gly Ile Ser Tyr Pro
41 1 5 10 15
43 att att caa ggc gga atg gcg aag att tcc aga cct gac ctg gtt tct      96
44 Ile Ile Gln Gly Gly Met Ala Lys Ile Ser Arg Pro Asp Leu Val Ser
45 20 25 30
47 gcc gtg agt caa gcg ggt ggc ttg ggt gtt ttg acc tcc atg ggg ctg      144
48 Ala Val Ser Gln Ala Gly Gly Leu Gly Val Leu Thr Ser Met Gly Leu
49 35 40 45
51 act ccc caa gag ttg agc cag gat atc cag gaa gtc caa aag cgg att      192
52 Thr Pro Gln Glu Leu Ser Gln Asp Ile Gln Glu Val Gln Lys Arg Ile
53 50 55 60
55 gat cag ccc ttt gcc gtc aac cta atg ctc cag caa gat aat att ttt      240
56 Asp Gln Pro Phe Ala Val Asn Leu Met Leu Gln Gln Asp Asn Ile Phe
57 65 70 75
59 gac ctc ctg gaa gtg atc aaa gaa gtg aaa ccc cct gtg gtg atg acc      288
60 Asp Leu Leu Glu Val Ile Lys Glu Val Lys Pro Pro Val Val Met Thr
61 80 85 90 95

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63 ggt gct ggc agt ccc aaa gct ttt gtc caa gat tta agg gat ttg gac      336
64 Gly Ala Gly Ser Pro Lys Ala Phe Val Gln Asp Leu Arg Asp Leu Asp
65              100              105              110
67 atc aag gtc atc cca gtc ctg tcg acg gtg agc cag gcc cag aaa atg      384
68 Ile Lys Val Ile Pro Val Leu Ser Thr Val Ser Gln Ala Gln Lys Met
69              115              120              125
71 gaa gcc tta ggg gtg gat gcc atc gta gta gaa ggt caa gaa gca ggt      432
72 Glu Ala Leu Gly Val Asp Ala Ile Val Val Glu Gly Gln Glu Ala Gly
73              130              135              140
75 ggt cac att ggt tgg acg tca acc atg gct agc ctg ccc cag gtg gtc      480
76 Gly His Ile Gly Trp Thr Ser Thr Met Ala Ser Leu Pro Gln Val Val
77              145              150              155
79 cag gct gtt gac att ccg gtt gta gcg gca ggc ggt atc ggg tca gga      528
80 Gln Ala Val Asp Ile Pro Val Val Ala Ala Gly Gly Ile Gly Ser Gly
81 160              165              170              175
83 cag gcc att gca gca gcg gaa tgt ctg gga gct tgt ggt gtt cag ttg      576
84 Gln Ala Ile Ala Ala Glu Cys Leu Gly Ala Cys Gly Val Gln Leu
85              180              185              190
87 ggg acc ttg ttt ttg tcg gct aaa gaa tgc ccc atc agt gac ctc tac      624
88 Gly Thr Leu Phe Leu Ser Ala Lys Glu Cys Pro Ile Ser Asp Leu Tyr
89              195              200              205
91 cgc aaa aaa tta ctg gcc tgc cag gac cag gac acc ctg gtt agt gaa      672
92 Arg Lys Lys Leu Leu Ala Cys Gln Asp Gln Asp Thr Leu Val Ser Glu
93              210              215              220
95 ctc cac ccg ggt ggc cgg gtt cgg agc tta aaa gct agc tgt caa gat      720
96 Leu His Pro Gly Gly Arg Val Arg Ser Leu Lys Ala Ser Cys Gln Asp
97              225              230              235
99 gac cct gac ctc ttg gcc aag gaa ggg gaa gcc ggc ctc cat tat gcc      768
100 Asp Pro Asp Leu Leu Ala Lys Glu Gly Glu Ala Gly Leu His Tyr Ala
101 240              245              250              255
103 ggg gaa gtg gca gga caa ata gac aat tta gcc aca gcc caa gaa att      816
104 Gly Glu Val Ala Gly Gln Ile Asp Asn Leu Ala Thr Ala Gln Glu Ile
105              260              265              270
107 gta gac cga ctt gta gcc caa tac caa tcg aca cta aaa aaa cta att      864
108 Val Asp Arg Leu Val Ala Gln Tyr Gln Ser Thr Leu Lys Lys Leu Ile
109              275              280              285
111 caa taa      870
112 Gln
115 <210> SEQ ID NO: 2
116 <211> LENGTH: 288
117 <212> TYPE: PRT
118 <213> ORGANISM: Alloiococcus otitidis
120 <400> SEQUENCE: 2
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122 1              5              10              15
124 Ile Gln Gly Gly Met Ala Lys Ile Ser Arg Pro Asp Leu Val Ser Ala
125              20              25              30
127 Val Ser Gln Ala Gly Gly Leu Gly Val Leu Thr Ser Met Gly Leu Thr
128              35              40              45

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130 Pro Gln Glu Leu Ser Gln Asp Ile Gln Glu Val Gln Lys Arg Ile Asp
131      50                      55                      60
133 Gln Pro Phe Ala Val Asn Leu Met Leu Gln Gln Asp Asn Ile Phe Asp
134 65                      70                      75                      80
136 Leu Leu Glu Val Ile Lys Glu Val Lys Pro Pro Val Val Met Thr Gly
137                      85                      90                      95
139 Ala Gly Ser Pro Lys Ala Phe Val Gln Asp Leu Arg Asp Leu Asp Ile
140                      100                      105                      110
142 Lys Val Ile Pro Val Leu Ser Thr Val Ser Gln Ala Gln Lys Met Glu
143                      115                      120                      125
145 Ala Leu Gly Val Asp Ala Ile Val Val Glu Gly Gln Glu Ala Gly Gly
146      130                      135                      140
148 His Ile Gly Trp Thr Ser Thr Met Ala Ser Leu Pro Gln Val Val Gln
149 145                      150                      155                      160
151 Ala Val Asp Ile Pro Val Val Ala Ala Gly Gly Ile Gly Ser Gly Gln
152                      165                      170                      175
154 Ala Ile Ala Ala Glu Cys Leu Gly Ala Cys Gly Val Gln Leu Gly
155                      180                      185                      190
157 Thr Leu Phe Leu Ser Ala Lys Glu Cys Pro Ile Ser Asp Leu Tyr Arg
158                      195                      200                      205
160 Lys Lys Leu Leu Ala Cys Gln Asp Gln Asp Thr Leu Val Ser Glu Leu
161      210                      215                      220
163 His Pro Gly Gly Arg Val Arg Ser Leu Lys Ala Ser Cys Gln Asp Asp
164 225                      230                      235                      240
166 Pro Asp Leu Leu Ala Lys Glu Gly Glu Ala Gly Leu His Tyr Ala Gly
167                      245                      250                      255
169 Glu Val Ala Gly Gln Ile Asp Asn Leu Ala Thr Ala Gln Glu Ile Val
170                      260                      265                      270
172 Asp Arg Leu Val Ala Gln Tyr Gln Ser Thr Leu Lys Lys Leu Ile Gln
173      275                      280                      285
176 <210> SEQ ID NO: 3
177 <211> LENGTH: 957
178 <212> TYPE: DNA
179 <213> ORGANISM: Alloiococcus otitidis
181 <220> FEATURE:
182 <221> NAME/KEY: CDS
183 <222> LOCATION: (85)..(954)
185 <400> SEQUENCE: 3
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189 cagtacccaa ttatccaggg tggg atg gcc cgg att agt aag cca gaa tta      111
190                      Met Ala Arg Ile Ser Lys Pro Glu Leu
191                      1                      5
193 gtc agt gct gtc agc agt gca ggt ggc cta ggc gtt tta acc tcg gtt      159
194 Val Ser Ala Val Ser Ser Ala Gly Gly Leu Gly Val Leu Thr Ser Val
195 10                      15                      20                      25
197 ggg gtg gat gca gcg ggt ttt cgg gcg gac atc cag gaa atc cgc cgt      207
198 Gly Val Asp Ala Ala Gly Phe Arg Ala Asp Ile Gln Glu Ile Arg Arg
199                      30                      35                      40
201 ttg acg gac aag ccc ttt ggg gtc aac ttg atg ttg cag ttg gac aac      255

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202 Leu Thr Asp Lys Pro Phe Gly Val Asn Leu Met Leu Gln Leu Asp Asn
203          45                      50                      55
205 att cct gaa ttg ttg gag gtt gtc aag gaa gaa aaa cca gcc gtt gtc      303
206 Ile Pro Glu Leu Leu Glu Val Val Lys Glu Glu Lys Pro Ala Val Val
207          60                      65                      70
209 tta act gga gcg ggg acc ccg aaa gac ttt gcc caa gac ttg caa gca      351
210 Leu Thr Gly Ala Gly Thr Pro Lys Asp Phe Ala Gln Asp Leu Gln Ala
211          75                      80                      85
213 ctt ggc atc aaa gtt atc ccg gtt gtc tct gcc gtc aag cat gcc aag      399
214 Leu Gly Ile Lys Val Ile Pro Val Val Ser Ala Val Lys His Ala Lys
215 90          95                      100                      105
217 aaa atg gaa gcc ttg ggt gtg gat gcc gta gta tgt gaa ggc caa gaa      447
218 Lys Met Glu Ala Leu Gly Val Asp Ala Val Val Cys Glu Gly Gln Glu
219          110                      115                      120
221 gct ggt ggt cac att ggg atc act tct acc atg gcc acc ctg ccc cag      495
222 Ala Gly Gly His Ile Gly Ile Thr Ser Thr Met Ala Thr Leu Pro Gln
223          125                      130                      135
225 gtg gtg caa gct gtt gat atg cca gtt att gct gct ggt gga atc ggg      543
226 Val Val Gln Ala Val Asp Met Pro Val Ile Ala Ala Gly Gly Ile Gly
227          140                      145                      150
229 tca ggc cag gcc att gct gca gca gaa tgt tta ggg gca tgc ggg gta      591
230 Ser Gly Gln Ala Ile Ala Ala Ala Glu Cys Leu Gly Ala Cys Gly Val
231          155                      160                      165
233 caa ata ggg acc ttg ttt ttg gca gca gaa gag tgt gcc att agc gag      639
234 Gln Ile Gly Thr Leu Phe Leu Ala Ala Glu Glu Cys Ala Ile Ser Glu
235 170          175                      180                      185
237 gcc tac cgc cag cag gtc att gat gct ggc gac caa gat acc att gtt      687
238 Ala Tyr Arg Gln Gln Val Ile Asp Ala Gly Asp Gln Asp Thr Ile Val
239          190                      195                      200
241 acc gga att agt acc ggt ggc cgg gtc agg tcc gtt gcc tct cct ttc      735
242 Thr Gly Ile Ser Thr Gly Gly Arg Val Arg Ser Val Ala Ser Pro Phe
243          205                      210                      215
245 ttg gct gaa ctc ttg gcc gat gaa tta aag ggg tta gac cct aaa gtt      783
246 Leu Ala Glu Leu Leu Ala Asp Glu Leu Lys Gly Leu Asp Pro Lys Val
247          220                      225                      230
249 ttc ttg gaa agg act caa gga tct tat ggc cgg gcc att gcc gga gaa      831
250 Phe Leu Glu Arg Thr Gln Gly Ser Tyr Gly Arg Ala Ile Ala Gly Glu
251          235                      240                      245
253 att gac caa ggg acc atc cag gct ggc gaa gta gca ggt caa gtt aaa      879
254 Ile Asp Gln Gly Thr Ile Gln Ala Gly Glu Val Ala Gly Gln Val Lys
255 250          255                      260                      265
257 gcc aag tct act gcc aaa gca atc att gac cgg ctc gtg gct gaa tac      927
258 Ala Lys Ser Thr Ala Lys Ala Ile Ile Asp Arg Leu Val Ala Glu Tyr
259          270                      275                      280
261 cag gaa acc gta gcc aag ttt cag agt taa      957
262 Gln Glu Thr Val Ala Lys Phe Gln Ser
263          285                      290
266 <210> SEQ ID NO: 4
267 <211> LENGTH: 290

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268 <212> TYPE: PRT
269 <213> ORGANISM: Alloiococcus otitidis
271 <400> SEQUENCE: 4
272 Met Ala Arg Ile Ser Lys Pro Glu Leu Val Ser Ala Val Ser Ser Ala
273 1 5 10 15
276 Gly Gly Leu Gly Val Leu Thr Ser Val Gly Val Asp Ala Ala Gly Phe
277 20 25 30
280 Arg Ala Asp Ile Gln Glu Ile Arg Arg Leu Thr Asp Lys Pro Phe Gly
281 35 40 45
284 Val Asn Leu Met Leu Gln Leu Asp Asn Ile Pro Glu Leu Leu Glu Val
285 50 55 60
288 Val Lys Glu Glu Lys Pro Ala Val Val Leu Thr Gly Ala Gly Thr Pro
289 65 70 75 80
292 Lys Asp Phe Ala Gln Asp Leu Gln Ala Leu Gly Ile Lys Val Ile Pro
293 85 90 95
296 Val Val Ser Ala Val Lys His Ala Lys Lys Met Glu Ala Leu Gly Val
297 100 105 110
300 Asp Ala Val Val Cys Glu Gly Gln Glu Ala Gly Gly His Ile Gly Ile
301 115 120 125
304 Thr Ser Thr Met Ala Thr Leu Pro Gln Val Val Gln Ala Val Asp Met
305 130 135 140
308 Pro Val Ile Ala Ala Gly Gly Ile Gly Ser Gly Gln Ala Ile Ala Ala
309 145 150 155 160
312 Ala Glu Cys Leu Gly Ala Cys Gly Val Gln Ile Gly Thr Leu Phe Leu
313 165 170 175
316 Ala Ala Glu Glu Cys Ala Ile Ser Glu Ala Tyr Arg Gln Gln Val Ile
317 180 185 190
320 Asp Ala Gly Asp Gln Asp Thr Ile Val Thr Gly Ile Ser Thr Gly Gly
321 195 200 205
324 Arg Val Arg Ser Val Ala Ser Pro Phe Leu Ala Glu Leu Leu Ala Asp
325 210 215 220
328 Glu Leu Lys Gly Leu Asp Pro Lys Val Phe Leu Glu Arg Thr Gln Gly
329 225 230 235 240
332 Ser Tyr Gly Arg Ala Ile Ala Gly Glu Ile Asp Gln Gly Thr Ile Gln
333 245 250 255
336 Ala Gly Glu Val Ala Gly Gln Val Lys Ala Lys Ser Thr Ala Lys Ala
337 260 265 270
340 Ile Ile Asp Arg Leu Val Ala Glu Tyr Gln Glu Thr Val Ala Lys Phe
341 275 280 285
344 Gln Ser
345 290
348 <210> SEQ ID NO: 5
349 <211> LENGTH: 957
350 <212> TYPE: DNA
351 <213> ORGANISM: Alloiococcus otitidis
353 <220> FEATURE:
354 <221> NAME/KEY: CDS
355 <222> LOCATION: (25)..(954)
357 <400> SEQUENCE: 5

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/501,282

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Output Set: N:\CRF4\07202004\J501282.raw

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date